Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 01:51:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094118.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_ERR2094118 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094118_1.fastq.gz ERR2094118_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 01:51:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094118.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	490,440
Mapped reads	409,022 / 83.4%
Unmapped reads	81,418 / 16.6%
Mapped paired reads	409,022 / 83.4%
Mapped reads, first in pair	205,086 / 41.82%
Mapped reads, second in pair	203,936 / 41.58%
Mapped reads, both in pair	406,278 / 82.84%
Mapped reads, singletons	2,744 / 0.56%
Secondary alignments	0
Supplementary alignments	1,716 / 0.35%
Read min/max/mean length	30 / 151 / 133.16
Duplicated reads (estimated)	407,633 / 83.12%
Duplication rate	46.92%
Clipped reads	77,102 / 15.72%

2.2. ACGT Content

Number/percentage of A's	16,370,913 / 27.41%
Number/percentage of C's	12,773,793 / 21.39%
Number/percentage of T's	17,120,720 / 28.66%
Number/percentage of G's	13,461,461 / 22.54%
Number/percentage of N's	630 / 0%

GC Percentage	43.92%

2.3. Coverage

Mean	0.0193
Standard Deviation	33.3636

2.4. Mapping Quality

Mean Mapping Quality	11.19

2.5. Insert size

Mean	5,666.9
Standard Deviation	664,870.72
P25/Median/P75	217 / 232 / 262

2.6. Mismatches and indels

General error rate	1.64%
Mismatches	943,436
Insertions	21,772
Mapped reads with at least one insertion	5.24%
Deletions	40,883
Mapped reads with at least one deletion	9.78%
Homopolymer indels	67.81%

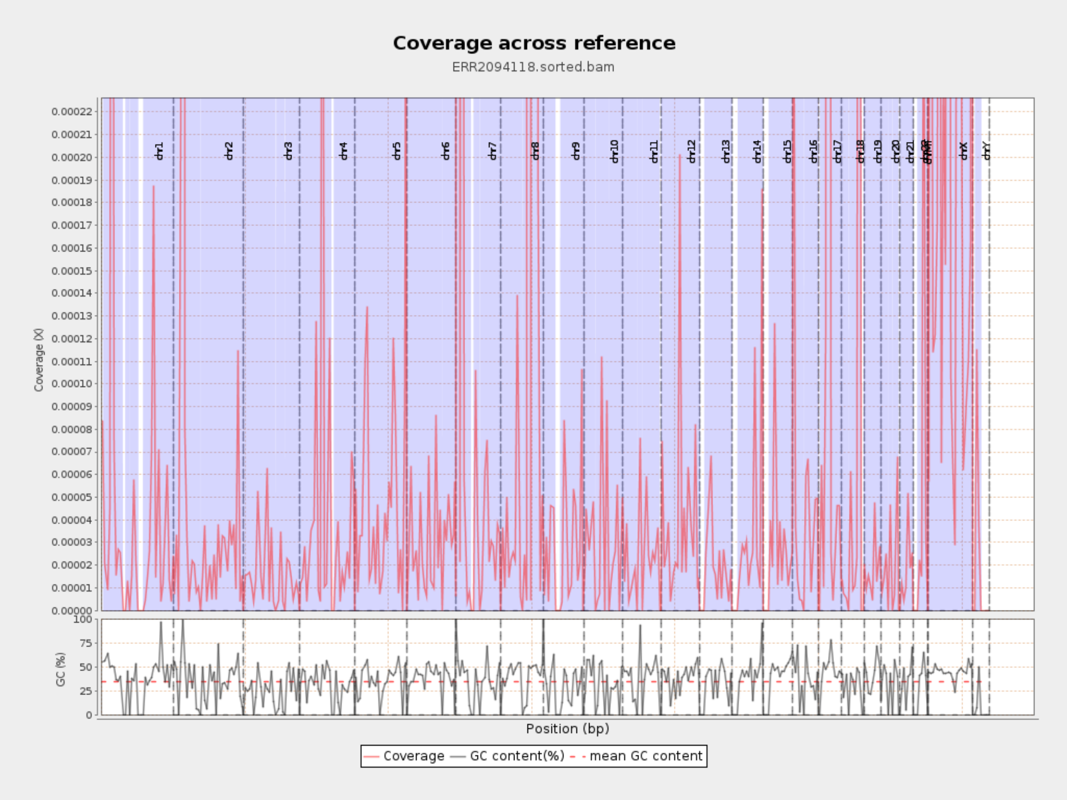
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

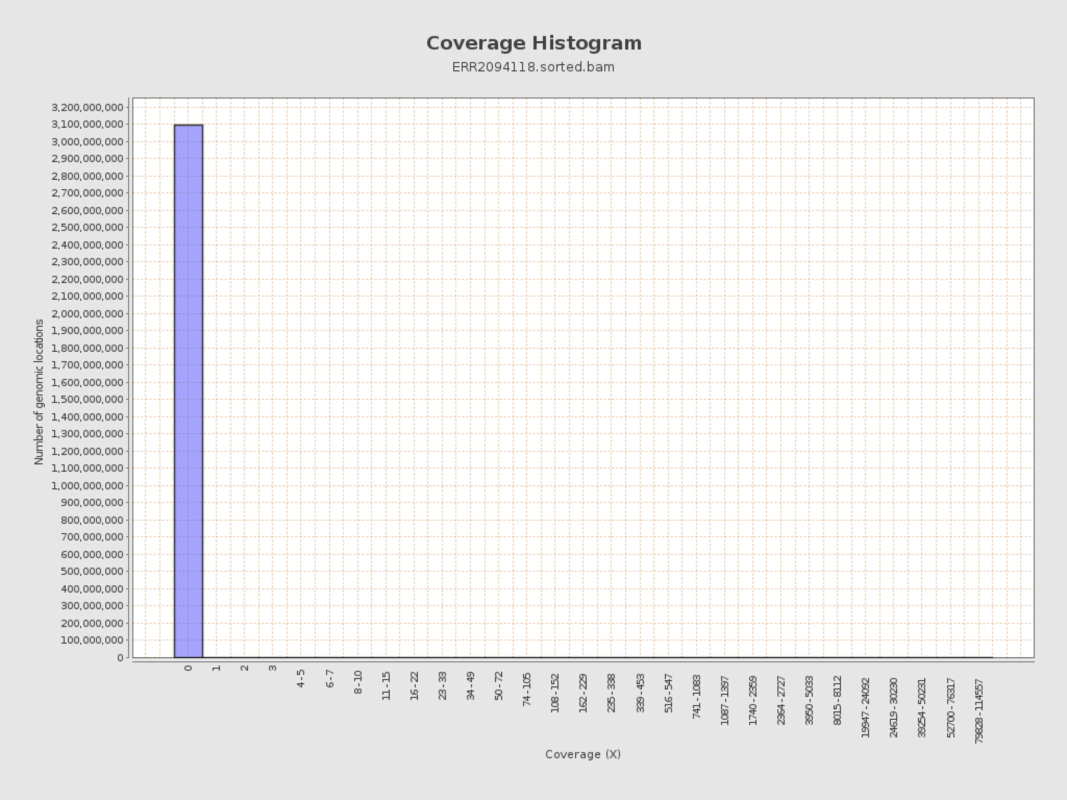
		bases	coverage	deviation
chr1	249250621	14032	0.0001	0.0344
chr2	243199373	242470	0.001	0.9569
chr3	198022430	3216	0	0.0045
chr4	191154276	8874	0	0.0219
chr5	180915260	8725	0	0.0137
chr6	171115067	5232	0	0.0098
chr7	159138663	79170	0.0005	0.7603
chr8	146364022	3568787	0.0244	9.8823
chr9	141213431	4152	0	0.011
chr10	135534747	4090	0	0.0113
chr11	135006516	3123	0	0.0089
chr12	133851895	5518	0	0.016
chr13	115169878	2159	0	0.0056
chr14	107349540	3803	0	0.0246
chr15	102531392	2726	0	0.0139
chr16	90354753	4273	0	0.0156
chr17	81195210	24868	0.0003	0.0871
chr18	78077248	9887	0.0001	0.0727
chr19	59128983	1091	0	0.0046
chr20	63025520	1294	0	0.005
chr21	48129895	875	0	0.0052
chr22	51304566	2947	0.0001	0.0452
chrMT	16571	55728874	3,363.0363	13,991.9375
chrX	155270560	43986	0.0003	0.152

chrY	59373566	1178	0	0.0128

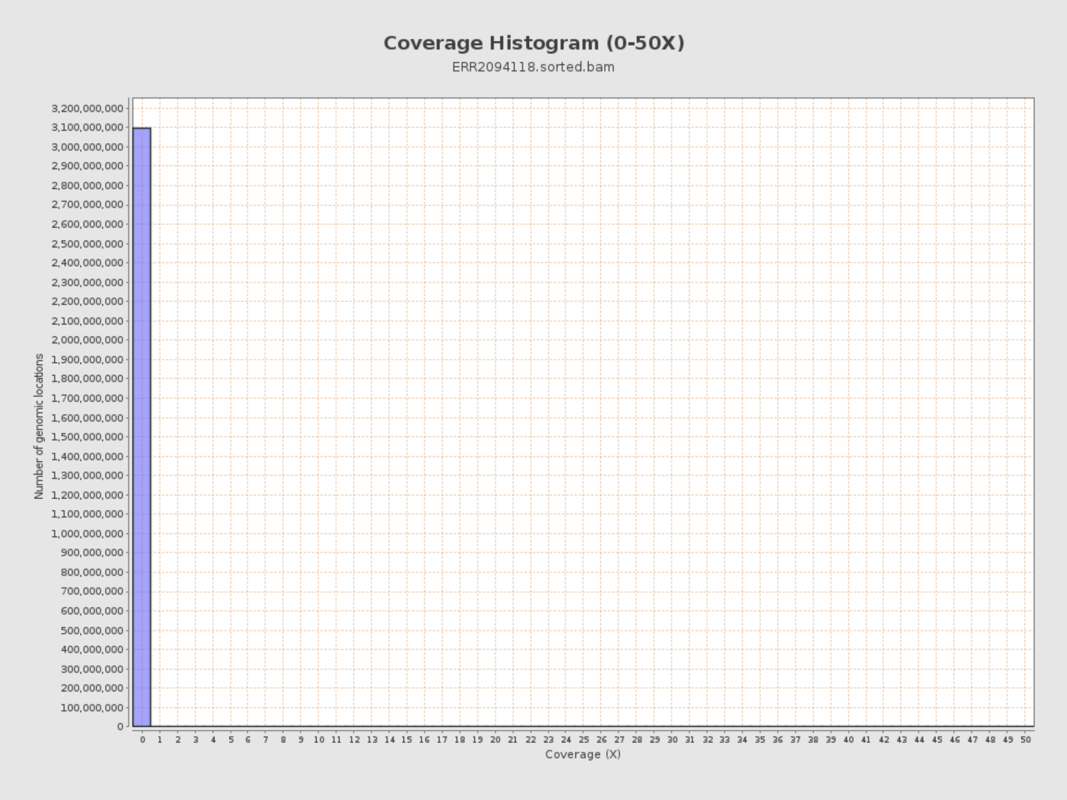
3. Results : Coverage across reference



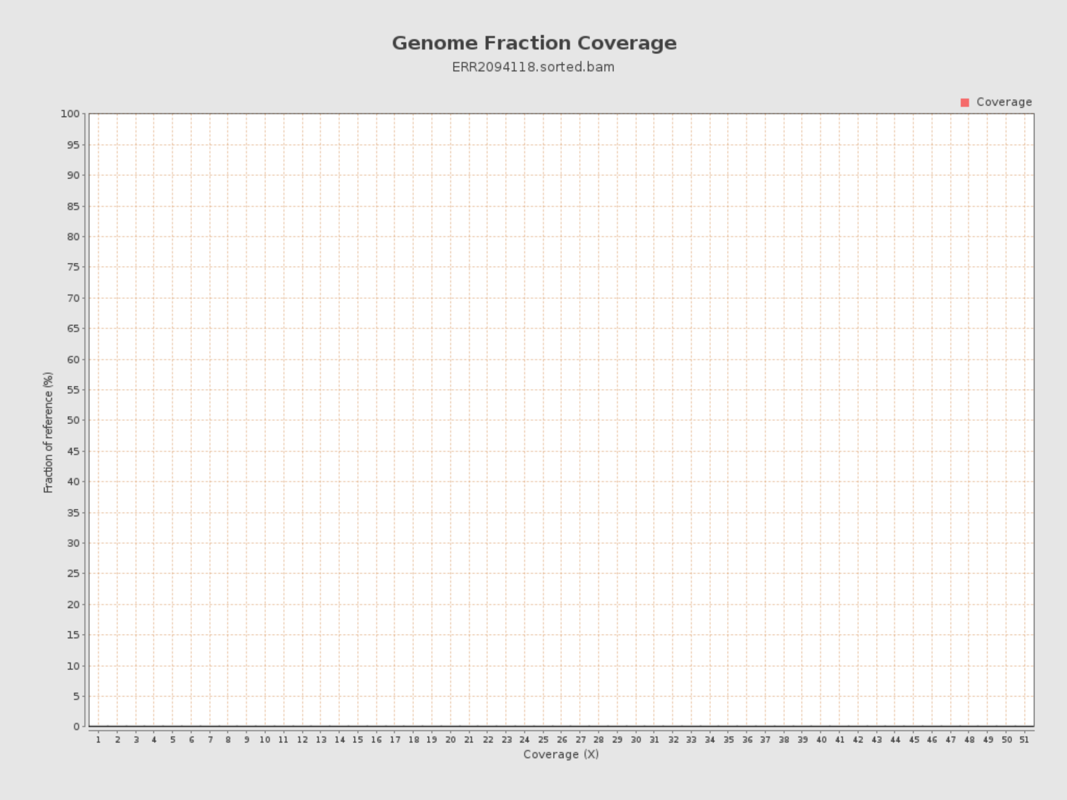
4. Results : Coverage Histogram



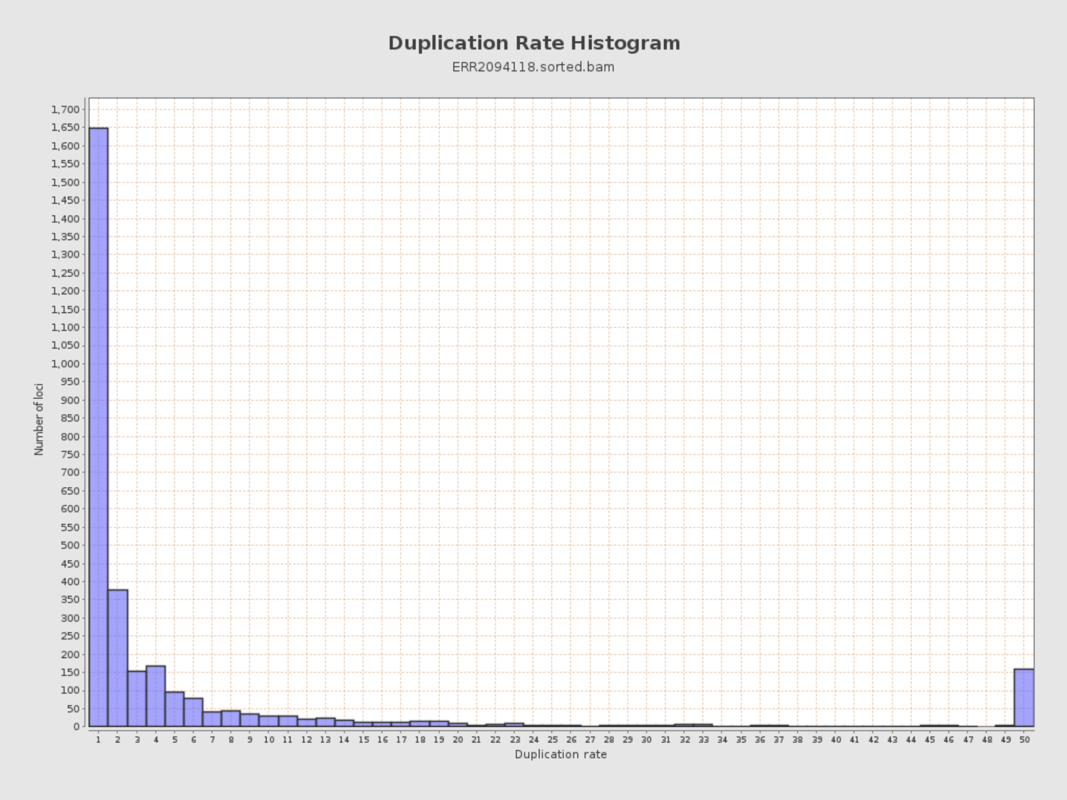
5. Results : Coverage Histogram (0-50X)



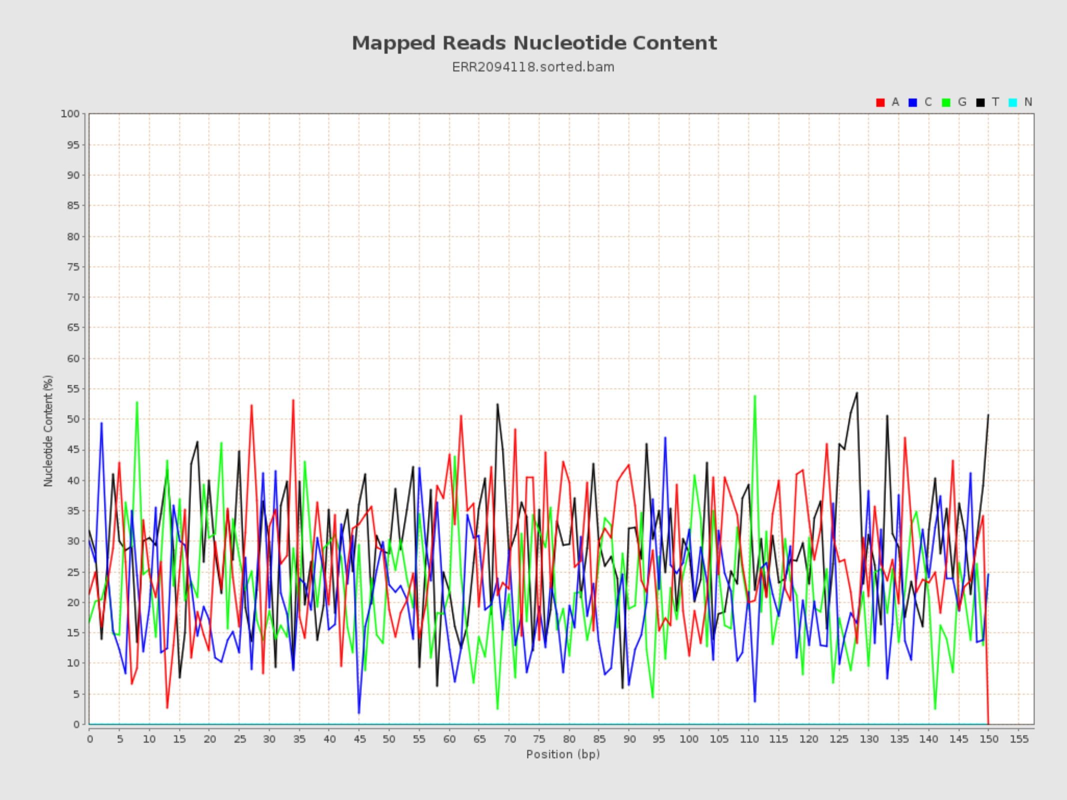
6. Results : Genome Fraction Coverage



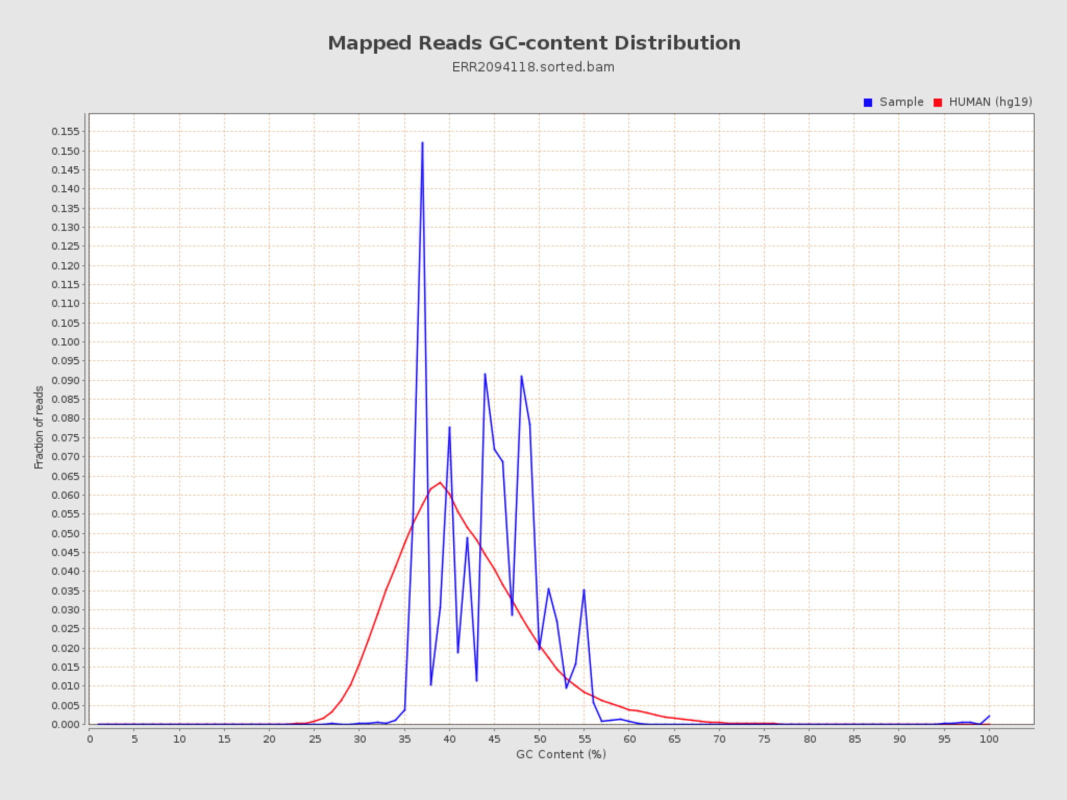
7. Results : Duplication Rate Histogram



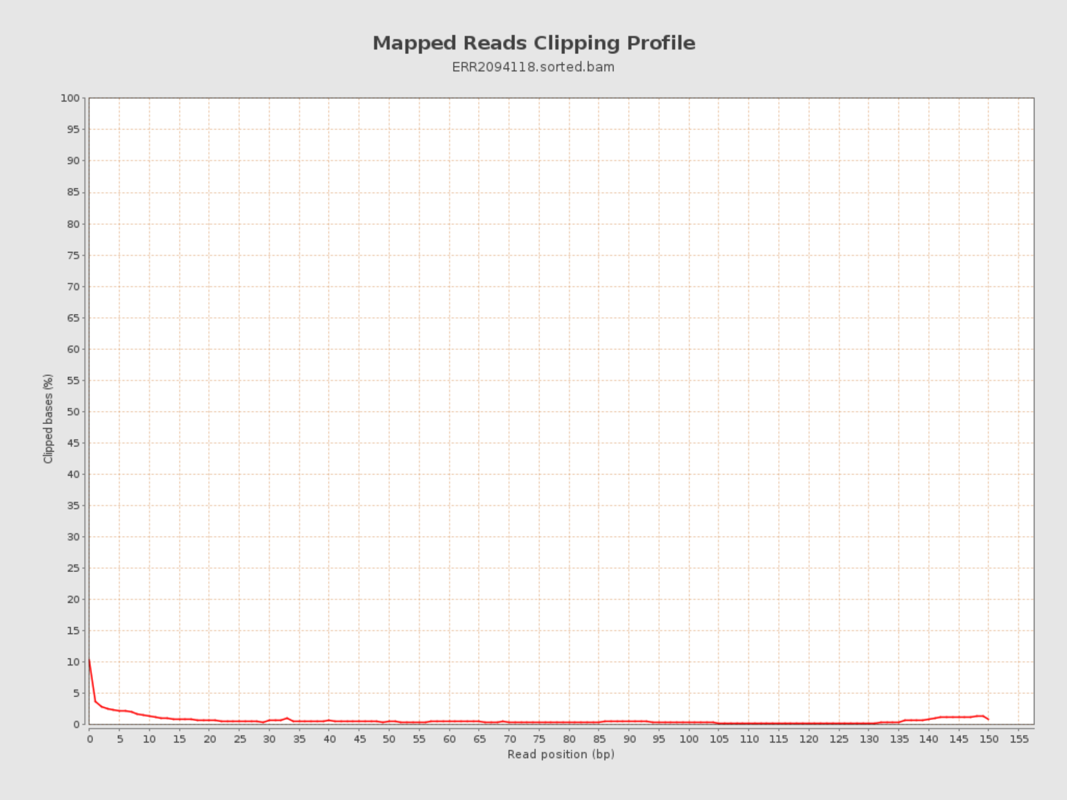
8. Results : Mapped Reads Nucleotide Content



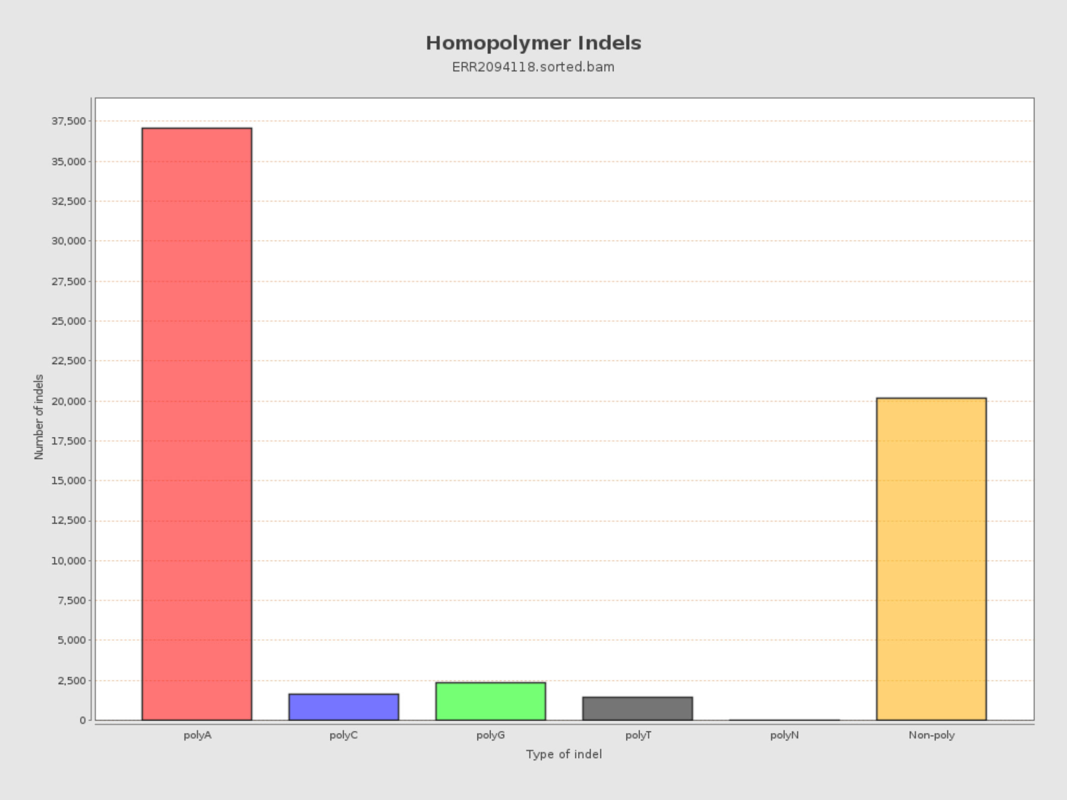
9. Results : Mapped Reads GC-content Distribution



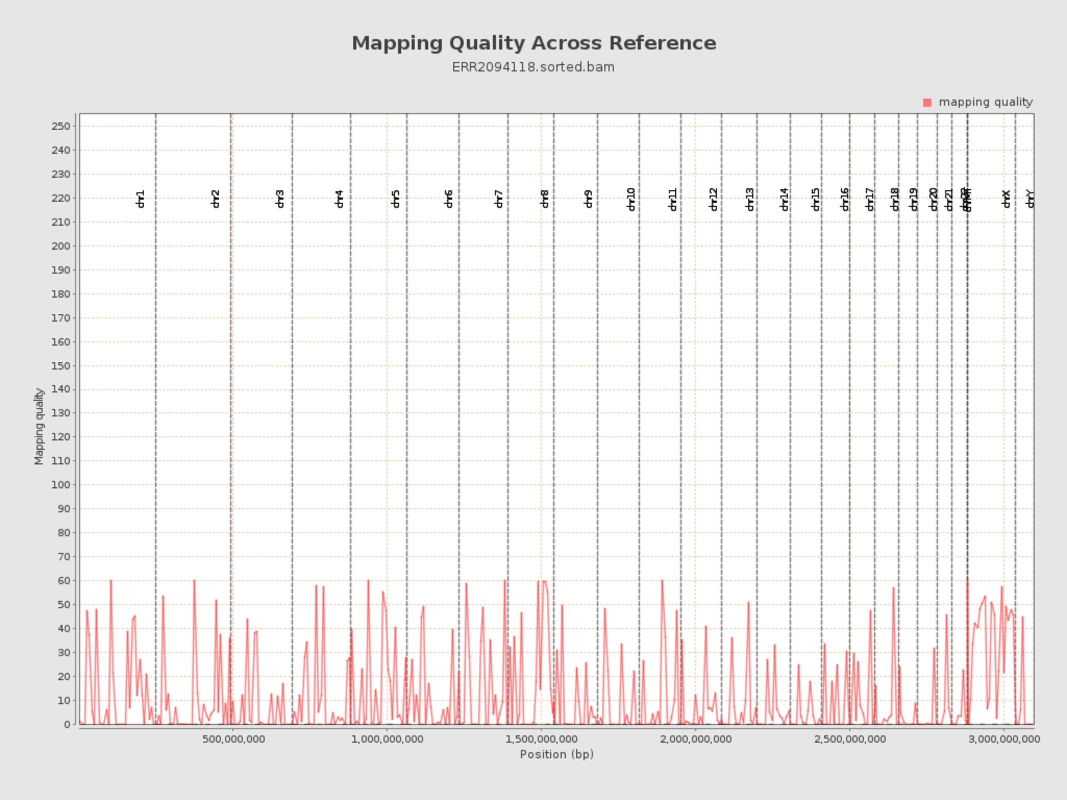
10. Results : Mapped Reads Clipping Profile



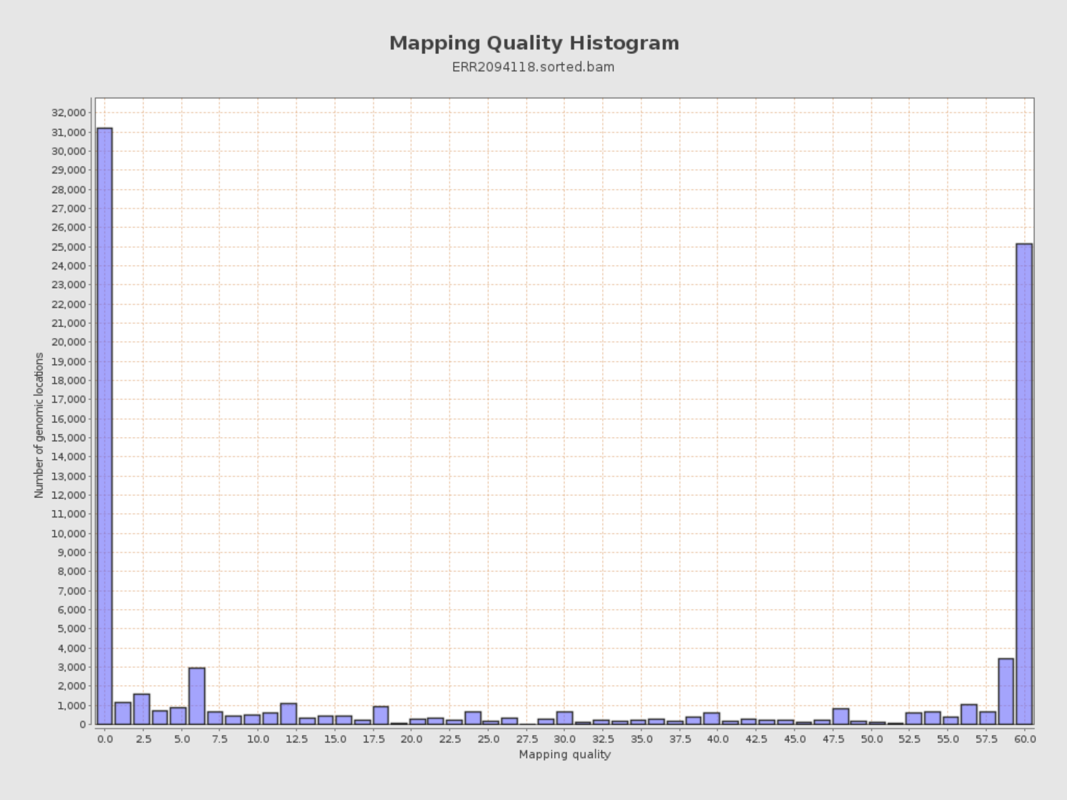
11. Results : Homopolymer Indels



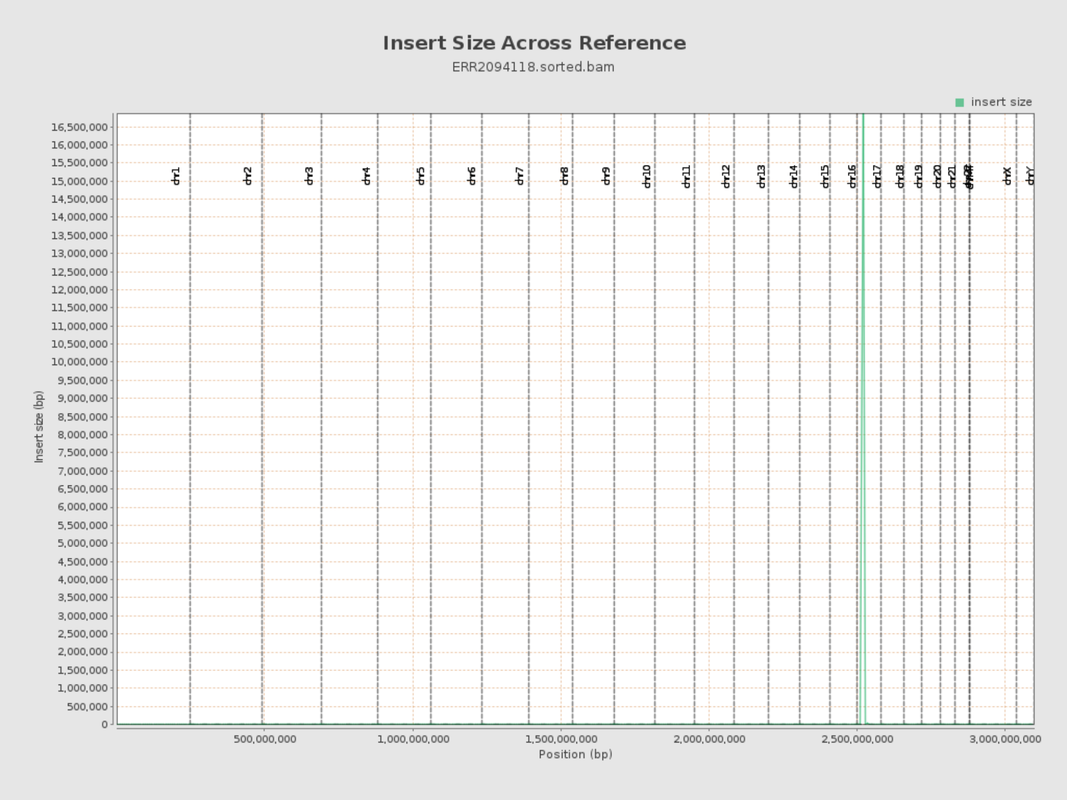
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram